SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LaVALLIE, EDWARD
RACIE, LISA

(ii) TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: GENETICS INSTITUTE, INC.
(B) STREET: 87 CAMBRIDGEPARK DRIVE
(C) CITY: CAMBRIDGE
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: LAZAR, STEVEN R.
(B) REGISTRATION NUMBER: 32,618

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 498-8260
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2027 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCC TTCATGGCCT AGCTCATTCT GCTCCCCCGG GTCGGAGCCC CCCGGAGCTG 60

CGCGCGGGCT TGCAGCGCCT CGCCCGCGCT CCTCCCGGTG TCCCGCTTCT CCGCGCCCCA 120

GCCGCCGGCT GCCAGCTTTT CGGGGCCCCG AGTCGCACCC AGCGAAGAGA GCGGGCCCGG 180

GACAAGCTCG AACTCCGGCC GCCTCGCCCT TCCCCGGCTC CGCTCCCTCT GCCCCCTCGG 240

GGTCGCGCGC CCACGATGCT GCAGGGCCCT GGCTCGCTGC TGCTGCTCTT CCTCGCCTCG 300

CACTGCTGCC TGGGCTCGGC GCGCGGGCTC TTCCTCTTTG GCCAGCCCGA CTTCTCCTAC 360

AAGCGCAGCA ATTGCAAGCC CATCCCGGCC AACCTGCAGC TGTGCCACGG CATCGAATAC 420

CAGAACATGC GGCTGCCCAA CCTGCTGGGC CACGAGACCA TGAAGGAGGT GCTGGAGCAG 480

GCCGGCGCTT GGATCCCGCT GGTCATGAAG CAGTGCCACC CGGACACCAA GAAGTTCCTG 540

TGCTCGCTCT TCGCCCCCGT CTGCCTCGAT GACCTAGACG AGACCATCCA GCCATGCCAC 600

TCGCTCTGCG TGCAGGTGAA GGACCGCTGC GCCCCGGTCA TGTCCGCCTT CGGCTTCCCC 660

TGGCCCGACA TGCTTGAGTG CGACCGTTTC CCCCAGGACA ACGACCTTTG CATCCCCCTC 720

GCTAGCAGCG ACCACCTCCT GCCAGCCACC GAGGAAGCTC CAAAGGTATG TGAAGCCTGC 780

AAAAATAAAA ATGATGATGA CAACGACATA ATGGAAACGC TTTGTAAAAA TGATTTTGCA 840

CTGAAAATAA AAGTGAAGGA GATAACCTAC ATCAACCGAG ATACCAAAAT CATCCTGGAG 900

ACCAAGAGCA AGACCATTTA CAAGCTGAAC GGTGTGTCCG AAAGGGACCT GAAGAAATCG 960

GTGCTGTGGC TCAAAGACAG CTTGCAGTGC ACCTGTGAGG AGATGAACGA CATCAACGCG 1020

CCCTATCTGG TCATGGGACA GAAACAGGGT GGGGAGCTGG TGATCACCTC GGTGAAGCGG 1080

TGGCAGAAGG GGCAGAGAGA GTTCAAGCGC ATCTCCCGCA GCATCCGCAA GCTGCAGTGC 1140

TAGTCCCGGC ATCCTGATGG CTCCGACAGG CCTGCTCCAG AGCACGGCTG ACCATTTCTG 1200

CTCCGGGATC TCAGCTCCCG TTCCCCAAGC ACACTCCTAG CTGCTCCAGT CTCAGCCTGG 1260

GCAGCTTCCC CCTGCCTTTT GCACGTTTGC ATCCCCAGCA TTTCCTGAGT TATAAGGCCA 1320

CAGGAGTGGA TAGCTGTTTT CACCTAAAGG AAAAGCCCAC CCGAATCTTG TAGAAATATT 1380

CAAACTAATA AAATCATGAA TATTTTTATG AAGTTTAAAA ATAGCTCACT TTAAAGCTAG 1440

TTTTGAATAG GTGCAACTGT GACTTGGGTC TGGTTGGTTG TTGTTTGTTG TTTTGAGTCA 1500

GCTGATTTTC ACTTCCCACT GAGGTTGTCA TAACATGCAA ATTGCTTCAA TTTTCTCTGT 1560

GGCCCAAACT TGTGGGTCAC AAACCCTGTT GAGATAAAGC TGGCTGTTAT CTCAACATCT 1620

TCATCAGCTC CAGACTGAGA CTCAGTGTCT AAGTCTTACA ACAATTCATC ATTTTATACC 1680

TTCAATGGGA ACTTAAACTG TTACATGTAT CACATTCCAG CTACAATACT TCCATTTATT 1740

AGAAGCACAT TAACCATTTC TATAGCATGA TTTCTTCAAG TAAAAGGCAA AAGATATAAA 1800

TTTTATAATT GACTTGAGTA CTTTAAGCCT TGTTTAAAAC ATTTCTTACT TAACTTTTGC 1860

AAATTAAACC CATTGTAGCT TACCTGTAAT ATACATAGTA GTTTACCTTT AAAAGTTGTA 1920

AAAATATTGC TTTAACCAAC ACTGTAAATA TTTCAGATAA ACATTATATT CTTGTATATA 1980

AACTTTACAT CCTGTTTTAC CTAAAAAAAA AAAAAAAAAG CGGCCGC 2027

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser His
1               5                  10                  15

Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln Pro Asp
            20                  25                  30

Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu Gln
        35                  40                  45

Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu
    50                  55                  60

Gly His Glu Thr Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile
65                  70                  75                  80

Pro Leu Val Met Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys
                85                  90                  95

Ser Leu Phe Ala Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln
            100                 105                 110

Pro Cys His Ser Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val
        115                 120                 125

Met Ser Ala Phe Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg
    130                 135                 140

Phe Pro Gln Asp Asn Asp Leu Cys Ile Pro Leu Ala Ser Ser Asp His
145                 150                 155                 160

Leu Leu Pro Ala Thr Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys
                165                 170                 175

Asn Lys Asn Asp Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn
            180                 185                 190

Asp Phe Ala Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg
        195                 200                 205

Asp Thr Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu
    210                 215                 220

Asn Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys
225                 230                 235                 240

Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala Pro
                245                 250                 255

Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile Thr Ser
            260                 265                 270

Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg Ile Ser Arg
        275                 280                 285

Ser Ile Arg Lys Leu Gln Cys
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln Pro Asp Phe Ser Tyr Lys
1               5                  10                  15

Arg Ser Asn Cys Lys Pro Ile Pro Ala Asn Leu Gln Leu Cys His Gly
            20                  25                  30

Ile Glu Tyr Gln Asn Met Arg Leu Pro Asn Leu Leu Gly His Glu Thr
        35                  40                  45

Met Lys Glu Val Leu Glu Gln Ala Gly Ala Trp Ile Pro Leu Val Met
    50                  55                  60

Lys Gln Cys His Pro Asp Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala
65                  70                  75                  80

Pro Val Cys Leu Asp Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser
                85                  90                  95

Leu Cys Val Gln Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe
            100                 105                 110

Gly Phe Pro Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp
        115                 120                 125

Asn Asp Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala
    130                 135                 140

Thr Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp
145                 150                 155                 160

Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala Leu
                165                 170                 175

Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr Lys Ile
            180                 185                 190

Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn Gly Val Ser
        195                 200                 205

Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys Asp Ser Leu Gln
    210                 215                 220

Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala Pro Tyr Leu Val Met
225                 230                 235                 240

Gly Gln Lys Gln Gly Gly Glu Leu Val Ile Thr Ser Val Lys Arg Trp
                245                 250                 255

Gln Lys Gly Gln Arg Glu Phe Lys Arg Ile Ser Arg Ser Ile Arg Lys
            260                 265                 270

Leu Gln Cys
        275
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